SEQUENCE LISTING

<110> Meyers, Rachel
       MacBeth, Kyle
       Tsai, Fong-Ying

<120> 8797, A NOVEL HUMAN
    GALACTOSYLTRANSFERASE AND USES THEREOF

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<151> 2000-08-31

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ttaaaactga tcctaactaa aaacagactt gagtggat atg aga atg ttg gtt agt 476
                                            Met Arg Met Leu Val Ser
                                             1   5

ggc aga aga gtc aaa aaa tgg cag tta att att cag tta ttt gct act   524
Gly Arg Arg Val Lys Lys Trp Gln Leu Ile Ile Gln Leu Phe Ala Thr
             10   15   20

tgt ttt tta gcg agc ctc atg ttt ttt tgg gaa cca atc gat aat cac   572
Cys Phe Leu Ala Ser Leu Met Phe Phe Trp Glu Pro Ile Asp Asn His
         25   30   35

att gtg agc cat atg aag tca tat tct tac aga tac ctc ata aat agc   620
Ile Val Ser His Met Lys Ser Tyr Ser Tyr Arg Tyr Leu Ile Asn Ser
     40   45   50

tat gac ttt gtg aat gat acc ctg tct ctt aag cac acc tca gcg ggg   668
Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu Lys His Thr Ser Ala Gly
 55   60   65   70

cct cgc tac caa tac ttg att aac cac aag gaa aag tgt caa gct caa   716
Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys Glu Lys Cys Gln Ala Gln
             75   80   85

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gac gtc ctc ctt tta ctg ttt gta aaa act gct cct gaa aac tat gat      764
Asp Val Leu Leu Leu Leu Phe Val Lys Thr Ala Pro Glu Asn Tyr Asp
            90                  95                 100

cga cgt tcc gga att aga agg acg tgg ggc aat gaa aat tat gtt cgg      812
Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly Asn Glu Asn Tyr Val Arg
        105                 110                 115

tct cag ctg aat gcc aac atc aaa act ctg ttt gcc tta gga act cct      860
Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu Phe Ala Leu Gly Thr Pro
        120                 125                 130

aat cca ctg gag gga gaa gaa cta caa aga aaa ctg gct tgg gaa gat      908
Asn Pro Leu Glu Gly Glu Glu Leu Gln Arg Lys Leu Ala Trp Glu Asp
135                 140                 145                 150

caa agg tac aat gat ata att cag caa gac ttt gtt gat tct ttc tac      956
Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp Phe Val Asp Ser Phe Tyr
                155                 160                 165

aat ctt act ctg aaa tta ctt atg cag ttc agt tgg gca aat acc tat     1004
Asn Leu Thr Leu Lys Leu Leu Met Gln Phe Ser Trp Ala Asn Thr Tyr
            170                 175                 180

tgt cca cat gcc aaa ttt ctt atg act gct gat gat gac ata ttt att     1052
Cys Pro His Ala Lys Phe Leu Met Thr Ala Asp Asp Asp Ile Phe Ile
            185                 190                 195

cac atg cca aat ctg att gag tac ctt caa agt tta gaa caa att ggt     1100
His Met Pro Asn Leu Ile Glu Tyr Leu Gln Ser Leu Glu Gln Ile Gly
        200                 205                 210

gtt caa gac ttt tgg att ggt cgt gtt cat cgt ggt gcc cct ccc att     1148
Val Gln Asp Phe Trp Ile Gly Arg Val His Arg Gly Ala Pro Pro Ile
215                 220                 225                 230

aga gat aaa agc agc aaa tac tac gtg tcc tat gaa atg tac cag tgg     1196
Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser Tyr Glu Met Tyr Gln Trp
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cca gct tac cct gac tac aca gcc gga gct gcc tat gta atc tcc ggt     1244
Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala Ala Tyr Val Ile Ser Gly
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gat gta gct gcc aaa gtc tat gag gca tca cag aca cta aat tca agt     1292
Asp Val Ala Ala Lys Val Tyr Glu Ala Ser Gln Thr Leu Asn Ser Ser
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ctt tac ata gac gat gtg ttc atg ggc ctc tgt gcc aat aaa ata ggg     1340
Leu Tyr Ile Asp Asp Val Phe Met Gly Leu Cys Ala Asn Lys Ile Gly
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ata gta ccg cag gac cat gtg ttt ttt tct gga gag ggt aaa act cct     1388
Ile Val Pro Gln Asp His Val Phe Phe Ser Gly Glu Gly Lys Thr Pro
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tat cat ccc tgc atc tat gaa aaa atg atg aca tct cat gga cac tta     1436
Tyr His Pro Cys Ile Tyr Glu Lys Met Met Thr Ser His Gly His Leu
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gaa gat ctc cag gac ctt tgg aag aat gct aca gat cct aaa gta aaa   1484
Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala Thr Asp Pro Lys Val Lys
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acc att tcc aaa ggt ttt ttt ggt caa ata tac tgc aga tta atg aag   1532
Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile Tyr Cys Arg Leu Met Lys
            345                 350                 355

ata att ctc ctt tgt aaa att agc tat gtg gac aca tac cct tgt agg   1580
Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val Asp Thr Tyr Pro Cys Arg
            360                 365                 370

gct gcg ttt atc taatagtact tgaatgttgt atgttttcac tgtcactgag       1632
Ala Ala Phe Ile
375

tcaaacctgg atgaaaaaaa cctttaaatg ttcgtctata ccctaagtaa aatgaggacg 1692
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Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr
        35                  40                  45
Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu
    50                  55                  60
Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys
65                  70                  75                  80
Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Leu Phe Val Lys Thr
            85                  90                  95
Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly
            100                 105                 110
Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu
            115                 120                 125
Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Glu Leu Gln Arg
    130                 135                 140
Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp
145                 150                 155                 160
Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe
            165                 170                 175
Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala
            180                 185                 190
Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln
            195                 200                 205
Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His
    210                 215                 220
Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser
225                 230                 235                 240
Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala
            245                 250                 255
Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser
            260                 265                 270
Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu
    275                 280                 285
Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser
    290                 295                 300
Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met
305                 310                 315                 320
Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala
            325                 330                 335
Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile
            340                 345                 350
Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val
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Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile
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att cag tta ttt gct act tgt ttt tta gcg agc ctc atg ttt ttt tgg    96
Ile Gln Leu Phe Ala Thr Cys Phe Leu Ala Ser Leu Met Phe Phe Trp
                20                  25                  30

gaa cca atc gat aat cac att gtg agc cat atg aag tca tat tct tac   144
Glu Pro Ile Asp Asn His Ile Val Ser His Met Lys Ser Tyr Ser Tyr
            35                  40                  45

aga tac ctc ata aat agc tat gac ttt gtg aat gat acc ctg tct ctt   192
Arg Tyr Leu Ile Asn Ser Tyr Asp Phe Val Asn Asp Thr Leu Ser Leu
        50                  55                  60

aag cac acc tca gcg ggg cct cgc tac caa tac ttg att aac cac aag   240
Lys His Thr Ser Ala Gly Pro Arg Tyr Gln Tyr Leu Ile Asn His Lys
65                  70                  75                  80

gaa aag tgt caa gct caa gac gtc ctc ctt tta ctg ttt gta aaa act   288
Glu Lys Cys Gln Ala Gln Asp Val Leu Leu Leu Leu Phe Val Lys Thr
                85                  90                  95

gct cct gaa aac tat gat cga cgt tcc gga att aga agg acg tgg ggc   336
Ala Pro Glu Asn Tyr Asp Arg Arg Ser Gly Ile Arg Arg Thr Trp Gly
            100                 105                 110

aat gaa aat tat gtt cgg tct cag ctg aat gcc aac atc aaa act ctg   384
Asn Glu Asn Tyr Val Arg Ser Gln Leu Asn Ala Asn Ile Lys Thr Leu
        115                 120                 125

ttt gcc tta gga act cct aat cca ctg gag gga gaa gaa cta caa aga   432
Phe Ala Leu Gly Thr Pro Asn Pro Leu Glu Gly Glu Glu Leu Gln Arg
    130                 135                 140

aaa ctg gct tgg gaa gat caa agg tac aat gat ata att cag caa gac   480
Lys Leu Ala Trp Glu Asp Gln Arg Tyr Asn Asp Ile Ile Gln Gln Asp
145                 150                 155                 160

ttt gtt gat tct ttc tac aat ctt act ctg aaa tta ctt atg cag ttc   528
Phe Val Asp Ser Phe Tyr Asn Leu Thr Leu Lys Leu Leu Met Gln Phe
                165                 170                 175

agt tgg gca aat acc tat tgt cca cat gcc aaa ttt ctt atg act gct   576
Ser Trp Ala Asn Thr Tyr Cys Pro His Ala Lys Phe Leu Met Thr Ala
            180                 185                 190

gat gat gac ata ttt att cac atg cca aat ctg att gag tac ctt caa   624
Asp Asp Asp Ile Phe Ile His Met Pro Asn Leu Ile Glu Tyr Leu Gln
        195                 200                 205

agt tta gaa caa att ggt gtt caa gac ttt tgg att ggt cgt gtt cat   672
Ser Leu Glu Gln Ile Gly Val Gln Asp Phe Trp Ile Gly Arg Val His
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Arg Gly Ala Pro Pro Ile Arg Asp Lys Ser Ser Lys Tyr Tyr Val Ser
225             230             235             240

tat gaa atg tac cag tgg cca gct tac cct gac tac aca gcc gga gct    768
Tyr Glu Met Tyr Gln Trp Pro Ala Tyr Pro Asp Tyr Thr Ala Gly Ala
                245             250             255

gcc tat gta atc tcc ggt gat gta gct gcc aaa gtc tat gag gca tca    816
Ala Tyr Val Ile Ser Gly Asp Val Ala Ala Lys Val Tyr Glu Ala Ser
            260             265             270

cag aca cta aat tca agt ctt tac ata gac gat gtg ttc atg ggc ctc    864
Gln Thr Leu Asn Ser Ser Leu Tyr Ile Asp Asp Val Phe Met Gly Leu
            275             280             285

tgt gcc aat aaa ata ggg ata gta ccg cag gac cat gtg ttt ttt tct    912
Cys Ala Asn Lys Ile Gly Ile Val Pro Gln Asp His Val Phe Phe Ser
    290             295             300

gga gag ggt aaa act cct tat cat ccc tgc atc tat gaa aaa atg atg    960
Gly Glu Gly Lys Thr Pro Tyr His Pro Cys Ile Tyr Glu Lys Met Met
305             310             315             320

aca tct cat gga cac tta gaa gat ctc cag gac ctt tgg aag aat gct    1008
Thr Ser His Gly His Leu Glu Asp Leu Gln Asp Leu Trp Lys Asn Ala
            325             330             335

aca gat cct aaa gta aaa acc att tcc aaa ggt ttt ttt ggt caa ata    1056
Thr Asp Pro Lys Val Lys Thr Ile Ser Lys Gly Phe Phe Gly Gln Ile
            340             345             350

tac tgc aga tta atg aag ata att ctc ctt tgt aaa att agc tat gtg    1104
Tyr Cys Arg Leu Met Lys Ile Ile Leu Leu Cys Lys Ile Ser Tyr Val
        355             360             365

gac aca tac cct tgt agg gct gcg ttt atc                            1134
Asp Thr Tyr Pro Cys Arg Ala Ala Phe Ile
    370             375
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